

SEQUENCE LISTING

<110> Meyers, Rachel A.
MacBeth, Kyle J.

<120> 14094, A NOVEL TRYPSIN FAMILY MEMBER AND
USES THEREFOR

<130> 10448-046002

<150> US 09/633,300

<151> 2000-08-08

<150> US 60/200,621

<151> 2000-04-28

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (628)...(1986)

<221> misc_feature

<222> (1)...(2948)

<223> n = A,T,C or G

<400> 1

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gtatttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact    180
gttaccact ttgcctcgtc ttcaccctgt ccaaacacog gtctccaatt tgcccttcag    240
agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca    300
ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc    360
caaactccaa aaaaaaaccc gaattcagcc tggttaagtc caagctgaat tccgggtggg    420
ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattagggtc atgcccgat    480
gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc    540
gtgggtgcat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg    600
gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt    654
                                Met Gly Glu Asn Asp Pro Pro Ala Val
                                1                                5

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gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa    702
Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
  10                      15                      20                      25

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ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg    750
Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
          30                      35                      40

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14094-046002

tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att	798
Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile	
45 50 55	
gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc	846
Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys	
60 65 70	
tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata	894
Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile	
75 80 85	
gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac	942
Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	
90 95 100 105	
cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca	990
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr	
110 115 120	
gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac	1038
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr	
125 130 135	
gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca	1086
Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser	
140 145 150	
gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt	1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe	
155 160 165	
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac	1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His	
170 175 180 185	
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc	1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr	
190 195 200	
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc	1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile	
205 210 215	
gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc	1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser	
220 225 230	
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc	1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro	
235 240 245	
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc	1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro	
250 255 260 265	
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca	1470

Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro
 270 275 280
 gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag 1518
 Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys
 285 290 295
 cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca 1566
 Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro
 300 305 310
 ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa 1614
 Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu
 315 320 325
 gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc 1662
 Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
 330 335 340 345
 aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc 1710
 Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val
 350 355 360
 cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc 1758
 Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly
 365 370 375
 atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg 1806
 Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val
 380 385 390
 gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg 1854
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg
 395 400 405
 agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca 1902
 Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala
 410 415 420 425
 gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac 1950
 Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp
 430 435 440
 tgg atc cac gag cag atg gag aga gac cta aaa acc tgaaaaggaa 1996
 Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr
 445 450
 ggggacaagt agccaccta gttcctgagg tgatgaagac agcccgatcc tcccctggac 2056
 tcccgtgtag gaacctgcac acgagcagac acccttgagg ctctgagttc cggcaccagt 2116
 agcaggcccc aaagaggcac ccttccatct gattccagca caaccttcaa gctgcttttt 2176
 gttttttgtt tttttgagat ggagtctcgc tctgttgccc aggetggagt gcagtggcga 2236
 aatccctgct cactgcagcc tccgcttccc tggttcaagc gattctcttg cctcagcttc 2296
 cccagtagct gggaccacag gtgcccgcga ccacacccaa ctaatttttg tatttttagt 2356
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 gcctgcttca gcctcccaca gtgctgggat tacaggcatg ggccaccacg cctagcctca 2476
 cgctcctttc tgatcttcac taagaacaaa agaagcagca acttgcaagg ggggcctttc 2536
 ccactgggtcc atctgggttt ctctccaggg gtcttgcaaa attcctgacg agataagcag 2596

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ttatgtgacc tcacgtgcaa agccaccaac agccactcag aaaagacgca ccagcccaga 2656
agtgcagaac tgcagtcact gcacgttttc atctctaggg accagaacca aaccaccct 2716
ttctacttcc aagacttatt ttcacatgtg gggagggttaa tctaggaatg actcgtttaa 2776
ggcctatttt catgatttct ttgtagcatt tgggtgcttga cgtattattg tcctttgatt 2836
ccaaataata tgttttccttc cctcatwraa maaaaaaaaa aaaaaaaarr rmrrssgcta 2896
vavmarktta gagaaaaaac ctaccacrc cttccccctg aamctraaam ya 2948

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<210> 2
<211> 453
<212> PRT
<213> Homo sapiens

```

```

<400> 2
Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg
 1      5      10      15
Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
 20      25      30
Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
 35      40      45
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
 50      55      60
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
 65      70      75      80
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
 85      90      95
Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
 100     105     110
Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
 115     120     125
Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
 130     135     140
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
 145     150     155     160
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
 165     170     175
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
 180     185     190
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
 195     200     205
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
 210     215     220
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
 225     230     235     240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
 245     250     255
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
 260     265     270
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
 275     280     285
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
 290     295     300
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
 305     310     315     320
Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
 325     330     335
Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala
 340     345     350

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```

Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile
      355              360              365
Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu
      370              375              380
Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
385              390              395              400
Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly
      405              410              415
Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val
      420              425              430
Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu
      435              440              445
Arg Asp Leu Lys Thr
      450

```

```

<210> 3
<211> 1362
<212> DNA
<213> Homo sapiens

```

```

<400> 3
atgggggaaa atgatccgcc tgcgtgttgaa gcccccttct cattccgata gctttttggc      60
cttgatgatt tgaaaataag tccgtgttgca ccagatgcag atgctgttgc tgcacagatc      120
ctgtcactgc tgccattgaa gttttttcca atcatcgtca ttgggatcat tgcattgata      180
ttagcactgg ccattgggtct gggcatccac ttgcactgct cagggaagta cagatgtcgc      240
tcatccttta agtgtatcga gctgatatgt cgatgtgacg gagtctcgga ttgcaaagac      300
ggggaggacg agtaccgctg tgtccgggtg ggtggtcaga atgccgtgct ccagggtgttc      360
acagctgctt cgtggaagac catgtgctcc gatgactgga agggtcacta cgcaaagtgt      420
gcctgtgccc aactgggttt cccaagctat gtgagttcag ataacctcag agtgagctcg      480
ctggaggggg agttccggga ggagtttgtg tccatcgatc acctcttgcc agatgacaag      540
gtgactgcat tacaccactc agtatatgtg agggagggat gtgcctctgg ccacgtgggt      600
accttgacgt gcacagcctg tggatcataga aggggctaca gctcacgcat cgtgggtgga      660
aacatgtcct tgcctcgcga gtggccctgg caggccagcc ttcagttcca gggctaccac      720
ctgtgcgggg gctctgtcat cacgcccctg tggatcatca ctgctgcaca ctgtgtttat      780
gacttgtacc tccccaaagtc atggaccatc cagggtgggtc tagtttccct gttggacaat      840
ccagcccatc cccacttggt ggagaagatt gtctaccaca gcaagtacaa gccaaagagg      900
ctgggcaatg acatcgccct tatgaagctg gccggggcac tcacgttcaa tgaaatgatc      960
cagcctgtgt gcctgcccac ctctgaagag aacttccccg atggaaaagt gtgctggacg      1020
tcaggatggg gggccacaga ggatggaggt gacgcctccc ctgtcctgaa ccacgcggcc      1080
gtccctttga tttccaacaa gatctgcaac cacagggacg tgtacgggtg catcatctcc      1140
ccctccatgc tctgcgcggg ctacctgacg ggtggcggtg acagctgcca gggggacagc      1200
ggggggcccc tgggtgtgtca agagaggagg ctgtggaagt tagtgggagc gaccagcttt      1260
ggcatcggct gcgcagaggt gaacaagcct ggggtgtaca cccgtgtcac ctccctcctg      1320
gactggatcc acgagcagat ggagagagac ctaaaaacct ga      1362

```

```

<210> 4
<211> 260
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> consensus sequence

```

```

<400> 4
Ile Val Gly Gly Arg Glu Ala Gln Pro Gly Ser Phe Gly Ser Pro Trp
1              5              10              15
Gln Val Ser Leu Gln Val Arg Ser Gly Gly Gly Ser Arg Lys His Phe

```

<400> 5															
Arg	Ile	Val	Gly	Gly	Ser	Glu	Ala	Lys	Ile	Gly	Ser	Phe	Pro	Trp	Gln
1				5					10					15	
Val	Ser	Leu	Gln	Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Arg	Trp	Val	Leu
			20					25					30		
Thr	Ala	Ala	His	Cys	Arg	Val	Arg	Leu	Gly	Ser	His	Asp	Leu	Ser	Ser
			35				40					45			
Gly	Glu	Glu	Thr	Glu	Gly	Gly	Pro	Arg	Leu	Asp	Ser	Pro	Gly	Gly	Gln
	50					55					60				
Val	Ile	Lys	Val	Ser	Lys	Ile	Ile	Glu	Val	His	Pro	Asn	Tyr	Asn	Asn
65					70					75				80	
Asp	Ile	Ala	Leu	Leu	Lys	Leu	Lys	Glu	Pro	Val	Thr	Leu	Ser	Asp	Ser
				85					90					95	
Asn	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro	Ser	Ser	Asn	Glu	Ile	Lys	Thr
			100					105					110		
Ser	Glu	Gly	Asn	Thr	Val	Pro	Ala	Gly	Thr	Thr	Cys	Thr	Val	Ser	Gly
		115					120					125			

```

Trp Gly Arg Thr Ser Glu Gly Pro Glu Glu Ser Gly Gly Gly Ser Leu
 130          135          140
Pro Asp Val Leu Gln Glu Val Asn Val Pro Ile Val Ser Asn Glu Thr
145          150          155          160
Cys Arg Met Leu Cys Ala Gly Tyr Leu Glu Gly Gly Asn Thr Pro Gly
          165          170          175
Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Val
          180          185          190
Leu Val Gly Ile Val Ser Trp Gly Ser Ser Ser Leu Tyr Gly Cys Ala
          195          200          205
Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr Leu Asp
          210          215          220
Trp Ile
225

```

```

<210> 6
<211> 43
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> consensus sequence

```

```

<400> 6
Ser Thr Cys Gly Gly Pro Asp Glu Phe Gln Cys Gly Ser Gly Arg Arg
 1          5          10          15
Cys Ile Pro Arg Ser Trp Val Cys Asp Gly Asp Pro Asp Cys Glu Asp
          20          25          30
Gly Ser Asp Glu Ser Leu Glu Asn Cys Ala Ala
          35          40

```

```

<210> 7
<211> 113
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> consensus sequence

```

```

<400> 7
Val Gly Gly Ser Ser Arg Cys Glu Gly Arg Val Glu Val Arg His Asp
 1          5          10          15
Gly Ser Lys Trp Gly Thr Val Cys Asp Ser Ser Trp Ser Leu Arg Asp
          20          25          30
Ala Asn Val Asp Pro Gln Ala Ser Lys Val Cys Arg Gln Leu Gly Cys
          35          40          45
Gly Gly Ala Val Ser Leu Leu Gly Pro Tyr Phe Ser Glu Gly Gly Gly
          50          55          60
Pro Ala Gly Gln Arg Glu Ile Trp Leu Asp Gly Val Asn Cys Ser Gly
          65          70          75          80
Asn Glu Thr Ser Leu Ser Gln Cys Pro Val Arg Val Thr Pro Pro Gly
          85          90          95
Leu Ser Arg Gln Cys Ser His Asp Gly Glu Asp Ala Gly Val Val Cys
          100          105          110
Ser

```

<400> 8
Arg Ile Val Gly Gly
1 5

<220>
<223> motif

```
<221> VARIANT
<222> 5
<223> Xaa = Gly or Ser
```

```
<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence
```

```
<221> VARIANT
<222> 1
<223> Xaa = Leu, Ile, Val, or Met
```

```
<221> VARIANT
<222> 4
<223> Xaa = Ser, Thr, Ala, or Gly
```

```
<210> 11
<211> 2951
<212> DNA
<213> Homo sapiens
```


gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca 1086

Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser	
140 145 150	
gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt	1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe	
155 160 165	
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac	1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His	
170 175 180 185	
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc	1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr	
190 195 200	
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc	1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile	
205 210 215	
gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc	1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser	
220 225 230	
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc	1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro	
235 240 245	
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc	1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro	
250 255 260 265	
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca	1470
Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro	
270 275 280	
gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag	1518
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys	
285 290 295	
cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca	1566
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro	
300 305 310	
ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa	1614
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu	
315 320 325	
gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc	1662
Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala	
330 335 340 345	
aca gag gat gga gca ggt gac gcc tcc cct gtc ctg aac cac gcg gcc	1710
Thr Glu Asp Gly Ala Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala	
350 355 360	
gtc cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt	1758
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly	

365	370	375	
ggc atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc			1806
Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly			
380	385	390	
gtg gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag			1854
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu			
395	400	405	
agg agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc			1902
Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys			
410	415	420	425
gca gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg			1950
Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu			
430	435	440	
gac tgg atc cac gag cag atg gag aga gac cta aaa acc tgaagaggaa			1999
Asp Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr			
445	450		
ggggacaagt agccacctga gttcctgagg tgatgaagac agcccgatcc tcccctggac			2059
tcccgtagtag gaacctgcac acgagcagac acccttggag ctctgagttc cggcaccagt			2119
agcaggcccc aaagaggcac ccttccatct gattccagca caaccttcaa gctgcttttt			2179
gttttttgtt tttttgagat ggagtctcgc tctgttgccc aggctggagt gcagtggcga			2239
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cccagtagct gggaccacag gtgcccgcga ccacacccaa ctaatttttg tatttttagt			2359
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gctgcttca gctcccaca gtgctgggat tacaggcatg ggccaccacg cctagcctca			2479
cgctcctttc tgatcttcac taagaacaaa agaagcagca acttgcaagg gcggcctttc			2539
ccactggtcc atctggtttt ctctccaggg gtcttgcaaa attcctgacg agataagcag			2599
ttatgtgacc tcacgtgcaa agccaccaac agccactcag aaaagacgca ccagcccaga			2659
agtgcagaac tgcagtcact gcacgttttc atctctaggg accagaacca aaccaccct			2719
ttctacttcc aagacttatt ttcacatgtg gggagggttaa tctaggaatg actcgtttaa			2779
ggcctatttt catgatttct ttgtagcatt tgggtgcttga cgtattattg tcctttgatt			2839
ccaaataata tgtttccttc cctcatwraa maaaaaaaaa aaaaaaaarr rmrrssgcta			2899
vavmarktta gagaaaaaac ctaccacacrc cttccccctg aamctraaam ya			2951

<210> 12

<211> 454

<212> PRT

<213> Homo sapiens

<400> 12

Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg	
1 5 10 15	
Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp	
20 25 30	
Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe	
35 40 45	
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala	
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